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1 MGSLFQEAEF QAGTEQNKPT LASRFQQTGLG DLLARLGSRG HVYVIHCLNP
51 TPGKIPGLLD VGHVAEQLRQ AGILEIIGTR STHFVVRVSF QVFLARFHAL
101 GSGRQKAASD QERCGAILSE VLGAESPLYH LGVTQVLLQE QGWQQLEQLW
151 AQRRSQALLT LHRGLRACIT RQRLRLPRM QARVRGLQAR KRYLQRRSAL
201 GQLNTILLVA RPLLRRLRQKL RCAPGPHSGE FWGKVSNMMDL GRLEIPAQLA
251 TLLERAEGHQ ALLTGSITES LPPEVPARPS LTLPPDIDQF PFSSFVSTSF
301 QKFPLPRPGQ PLDEPLTRLG GENPQQALEI NRVMRLRLGE GSLQSWQEQT
351 MGTFLVQQAQ RRPGLRDELF SQLVAQLWRN PDEQQNQRGW ALMVILLSSF
401 APTPALEKPL LKFVSDQAPS GMAALCQHKL LGALEQTPLA PMASRSHPTT
451 QLEWKAGLRR GRMALDVFTF NEESYSAEVE SWTTGEQFAG WILQSRGLEA
501 PPRGWSVSLH SGDAWRDLPG CDFVLDLIGQ TEDLGDPAGP HNPYITPLGL
551 AESIPPAPGV QAPSLPPGLP PGPAPILASS RPPGEASKPE NLDGFVDHLF
601 EPALAPGFSD LEQGWALSRR MKGGGSVGPT QQGYPMVYPG MVQAPSYQPA
651 MIPAPMPVMP AMGAVPTMPA MMVPPQPQFL VPSLDSRQLA LQQQNFINQQ
701 AMILAQQMTT QAMSLSLEQQ NQRHQHQAQT SGATSQPPPS TTAPKAKKPP
751 APQEKESNL EPSGVGLRED TPEEAESKPQ RPKSFQKRD YFQKMGQDPI
801 RVKTVKPPAK VQIPQEEMEE TEEEDETAEL SPFFFFFFV YKKPLKASRP
851 KAVKEDEAEF AQEEVPTQGE DPPVHSSNSA PQHPKPSRVP PVQSSNSAPP
901 RPQPSREIRN IIRMYQSRPG EVAVPVQPTR PIKTFQKND PKDEALAKLG
951 INGVHLPLST SPNQGKSSPP AVVPRPKARP RLEPSLSIQE KQGPLRDLFG
1001 PCSPNPPTAP APPPPPALPP PLSGEPKTPS VESHALTEPM EDKNISTKLL
1051 VPSGSVCFSY ANAPWKLFLR KEVFYPRENF SHPYCLSLLC QQILRDTFTE
1101 SCTRISQDER HKMKGLLGDL EVSLETLDIV EDSIKKRIVV AARDNWANYF

FIG. 1A.

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1151 SRIFPVSGES GSDVQLLGVS HRGLRLLKVT QSPSFHLDQL KTLCSYSYAE
1201 VLTVQCRGRS TLELSLKNEQ LILHTAWARA IKAMVDLFLS ELRKDSGYVI
1251 ALRSYITDDN SLLSFHRGDL IRLLPVTALE PGWQFGSAGG RSGLFPDDVV
1301 QPAAAPDLSF SLGKRNSWQR KSKLGPAQEV RKTEEVK*

FIG. 1B.

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1 CGCTGGGACT GTCACCTACC AGGTGCACAA GTTCATAAAC AGAAACAGGG
51 GCCACCTGGA CCCCCTGTG CTGGAGATGC TCAGGCAGAG CCAGCTGCAG
101 GTGACCTAGC CTTCTTTTCA GCTCATGGGC AGCCTGTTC AAGAAGCAGA
151 GCCCCAGGCT GGGACTGAGC AAAACAAACC CACATTGGCC TCTCGATTCC
201 AGCAGACCCT GGGTGA CTGACTCGGC TAGGCAGCAG GGGCCATGTC
251 TACGTATCC ACTGTCTCAA TCCCACCCT GGAAGATCC CAGGCCTCTT
301 GGACGTGGG CATGTGGCAG AGCAGCTGCG TCAGGCTGGC ATCCTGGAGA
351 TCATAGGCAC CCGGAGTACC CACTTCCCCG TGCAGGTGTC CTTCCAAGTC
401 TTTCTGGCAA GGTTCATGC CCTGGGTGTC GGGAGACAGA AAGCTGCCTC
451 TGACCAGGAG AGGTGTGGT CCATCCTCAG TGAAGTGCTG GGGGCAGAGT
501 CACCGCTGTA TCATCTTGA GTCACCCAGG TCCTGCTGCA GGAACAGGGC
551 TGGCAGCAGC TAGAACAGCT GTGGGCTCAG CGGCGCTCAC AGGCCCTGCT
601 CACTCTGCAC CGTGGCCTCC GAGCCTGTAT CACCCGGCAG CGCCTCCGTC
651 TCCTGCCCCG GATGCAGGCT CGTGTGCGTG GGCTCCAGGC CAGGAAGCGA
701 TATCTCCAGC GGAGGTCAGC TCTGGGACAG CTGAACACCA TTCTCCTAGT
751 GGCCCGGCCC CTGCTCCGGA GACGACAGAA GCTACGGTGT GCCCCTGGCC
801 CGCACAGCGG GGAGCCCTGG GGGAAAGTGT CAAATATGGA CCTGGGTCGC
851 TTAGAGATCC CCGCCAGCT GGCTACTCTG CTGGAGAGGG CGGAAGGCCA
901 CCAGGCCTTG CTGACGGGGA GCATCACAGA GTCCCTGCCA CCTGAGGTCC
951 CCGCCCGGCC CAGCCTGACT CTCCTCCAG ACATTGACCA GTTTCCTTC
1001 TCCAGTTTTG TATCCACCAG CTTTCAGAAG CCATTTCTGC CTCGACCAGG
1051 GCAGCCACTG GACGAGCCCC TGACGCGGTT AGATGGCGAG AACCCCTCAGC

FIG. 2A.

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1101 AGGCTCTGGA GATCAACAGG GTGATGCTGC GGCTCCTGGG GGAAGGATCT
1151 CTGCAGTCCT GGCAAGAGCA GACCATGGGC ACGTTCCTCG TGCAGCAGGC
1201 CCAGCGACGG CCGGGACTCC GAGATGAGCT CTTCAGCCAG CTGGTGGCCC
1251 AGCTGTGGCG CAACCCAGAT GAGCAACAGA ATCAGCGTGG CTGGGCCCCA
1301 ATGGTGATCC TGCTCAGCTC CTTTGCTCCC ACACCTGCCC TGGAGAAGCC
1351 ACTGCTCAA TTTGTATCTG ACCAGGCTCC CAGTGGCATG GCAGCCCTGT
1401 GCCAGCACAA GCTGTTAGGT GCCCTGGAGC AGACACCGCT GGCTCCCATG
1451 GCTTCGAGGT CCCACCCACC CACACAACT GAGTGAAGG CTGGTTTACG
1501 TCGGGGCCGC ATGGCGCTGG ATGTGTTTAC ATTCAACGAG GAAAGCTACT
1551 CCGCGGAAGT GGAATCCTGG ACCACGGGAG AGCAGTTTGC AGGGTGGATC
1601 CTACAGAGCA GAGGCCTGGA GCGCCCCCT CGTGCGTGGT CTGTGTCACT
1651 GCATTCTGGG GATGCTTGGC GTGACTTGCC TGGCTGTGAC TTTGTGTTGG
1701 ACCTAATAGG CCAGACTGAG GACTTGGGAG ACCCAGCTGG TCCCCACAAC
1751 TACCCCATCA CTCCTCTTGG TTTAGCTGAG AGCATCCCTC CAGCCCCCTGG
1801 TGTCCAGGCT CCTTCCCTGC CCCCAGGACT CCCTCCAGGT CCAGCCCCAA
1851 TACTGGCCAG CAGCCGCCCT CCGGGCGAGG CCAGTAAGCC TGAGAACCTG
1901 GATGGTTTCG TGGACCACCT CTTTGAACCA GCGCTCGCTC CGGGTTTCAG
1951 TGATCTGGAA CAAGGCTGGG CCCTGAGCAG ACGCATGAAG GGAGGGGGCT
2001 CTGTTGGGCC CACCCAGCAG GGCTACCCCA TGGTGTACCC AGGTATGGTG
2051 CAGGCACCTA GCTACCAGCC AGCTATGATA CCCGCACCGA TGCCCGTCAT
2101 GCCAGCCATG GCGCAGTCC CAACCATGCC AGCCATGATG GTGCCACCCC
2151 AGCCACAGCC TCTGGTGCCC AGTTTGGACT CAAGGCAGCT GGCCTACAG
2201 CAGCAAACT TCATCAACCA GCAGGCGATG ATTCTGGCGC AGCAGATGAC
2251 CACCCAGGCC ATGAGCTGT CCCTGGAGCA GCAGAATCAG AGACACCAGC

FIG. 2B.

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2301 ACCAAGCTCA GACCTCTGGG GCCACCTCCC AGCCTCCACC CTCAACCACT
2351 GCTCCCAAGG CCAAGAAGCC TCCTGCCCCC CAAGAGAAGC CAGAGAGTAA
2401 CCTAGAGCCT TCGGGTGTTG GCTTGAGAGA GGACACCCCA GAGGAAGCTG
2451 AAAGCAAGCC TCAGCGCCCC AAGAGCTTCC AACAGAAACG GGACTATTTT
2501 CAGAAGATGG GGCAAGATCC GATCAGAGTG AAGACGGTGA AACCTCCAGC
2551 CAAGGTTTCAG ATCCCCCAAG AGGAGATGGA GGAGACGGAG GAGGAGGAGG
2601 ATGAGACCGC CGAGTTGTCC CCTCCTCCTC CCCCTCCCCC GGTGTGTAAG
2651 AAGCCGCTGA AGGCAAGCAG GCCCAAAGCC GTAAAGGAAG ATGAGGCAGA
2701 GCCCGCCCAG GAGGAAGTAC CGACCCAGGG CGAGGATCCC CCGGTGCACA
2751 GCTCCAATC CGCACCTCAG CACCCCAAAC CCAGCAGGGT ACCCCCACTG
2801 CAGAGCTCCA ACTCCGCACC TCCACGCCCG CAACCCAGCA GGGAAATCCG
2851 AAACATCATC CGAATGTACC AGAGCCGTCC AGGGCCTGTG GCTGTGCCCC
2901 TACAACCCAC CAGGCCCATC AAAACTTTTC AGAAGAAAAA TGACCCTAAG
2951 GATGAGGCTT TGCTAAGTT AGGGATAAAT GGCGTCCACT TGCCCCATC
3001 GACATCGCCT AACCAAGGGA AGAGCTCTCC ACCGGCTGTA GTTCCTCGAC
3051 CTAAGGCTCG ACCTCGTCTT GAGCCTTCCC TATCCATCCA GGAAAAGCAG
3101 GGACCCCTTC GGGACTTGTT TGGCCCATGT AGTCCAAACC CACCTACAGC
3151 TCCAGCACCC CCGCCTCCAC CAGCACTCCC ACCGCCTCTG TCTGGGGAGC
3201 CCAAGACCCC TTCAGTGGAG TCTCATGCCT TGACAGAGCC CATGGAGGAC
3251 AAGAACATCT CCACAAAGCT CCTTGTGCCC TCTGGAAGTG TGTGCTTCTC
3301 CTATGCCAAT GCACCCTGGA AGTTGTTCTT ACGCAAGGAG GTGTTCTACC
3351 CCCGGGAGAA CTTCACTCAT CCATACTGCC TCAGTCTCCT CTGCCAGCAG
3401 ATCCTGCGGG ACACCTTCAC AGAGTCCTGC ACCCGGATCT CACAGGATGA

FIG. 2C.

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3451 GCGGCACAAA ATGAAAGGCC TTCTGGGAGA CTTGGAGGTG AGTCTGGAGA
3501 CCCTTGACAT TGTGTAAGAC AGCATCAAAA AACGCATCGT GGTCTGCTGT
3551 CGGGACAAC TGGCCAAATTA CTTCTCCCGC ATCTTCCCAG TCTCGGGTGA
3601 GAGTGGCAGC GATGTACAGC TGCTGGGTGT GTCTCACC GGACTGCGGC
3651 TGCTGAAGGT GACCCAAAGC CCGAGCTTCC ACCTGGACCA GCTGAAGACA
3701 CTCTGTTTCT ACAGCTATGC TGAAGTCCTG ACCGTGCAGT GCAGGGGCAG
3751 ATCCACCCTG GAGCTGTCCT TGAAGAATGA GCAGCTGATA CTGCACACAG
3801 CCTGGGCGAG GGCCATCAAG GCCATGGTGG ATCTATTCT GAGTGAAC T
3851 AGGAAGGACT CCGGCTATGT CATCGCCCTG CGCAGCTACA TCACCGATGA
3901 CAATAGCCTC CTCAGTTTCC ACCGTGGGGA CCTCATTAG TTA CTGCCAG
3951 TGACCGCTCT GGAAC CAGGC TGGCAGTTTC GTTCTGCCGG GGGCCGCTCC
4001 GGACTCTTTC CCGATGACGT GGTGCAGCCA GCTGCTGCCC CCGACCTCTC
4051 CTTTTCCCTG GGAAGAGAA ACAGCTGGCA ACGCAAGAGT AAGCTGGGGC
4101 CAGCTCAGGA GGTGAGGAAG ACAGAAGAGG TGAAGTGATA CAGGCCTAAC
4151 TTGGAGACTG AGAAGGAAAG AGCAGGGTTG CTTGGGTGT TGTCCACTTC
4201 CTGTCCTGGT GGCCAGGGCT CAATGTGTTT CTGTCCTTTA CCATCTCCTG
4251 ACTTTTGGCC ATTTGTGAGA CTGTAAGTCA CACCCTCTAA CTCTGGTACT
4301 TAGTTTCAGT TCTCCATAGA GGATGCTTAA TAAATAACCT TGGTTTTCTC
4351 GGTTCCTGGT GTCATCCTC TTGGGTCTAA TGGGTATGGG GACCAGGGCC
4401 TGAGAGTGAG TATTGGGCCT CTGGGCTAGA TGGTGGGTAC TGGGTGGTA
4451 CCAAATTTC TGTGCTCCCA GCGCCCCACC CATCCCAGGA AACAGAACC
4501 CAGTGAAGAC TCGGAGGCCA CCTCCTTAC AACCTACAGC TCTTTGTCTG
4551 CCGACCCCA CAACTACACC ATGCAGGAAT TTGCCCTGCG CTATTTCCGG
4601 AAGCTCATA CCTGGCTGAC CCAGATGAGT AGAGACACCA AAGAGAAAGC

FIG. 2D.

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4651 TGCCATCAAC CTGATCCAGT AACTAAGGA CCCATCCAG GAATCCCTTA
4701 CCAGCTTCTG CAATGGGGAC ACAAACAGTA AAGCTGTGGC TGGCTTCAAG
4751 GCTCTGATGC AGTTTATGGG GGACCAGCCT AAGCCCCGGG GCAAGGACGA
4801 GCTGAGTCTG CTCTATGAGC TGCTGAAGCT GTGCCAAGAT GACCTTAGGG
4851 ACGAGATGTA CTGCCAGGTC ATCAAGCAAG TCACAGGACA CCCCCAGCCA
4901 AAGCACTGTG CTCTGGGCTG GAGCGTCCTC AGCCTCTTCA CAGGCTTCTT
4951 TGCACCATCG ACCACGCTGA TGCCCTATGT GACCAAGTTC CTGCAGGATT
5001 CCAGCCCCAG TGAAGAGTTG GCCAGGAGGA GCCAGGAGAA CCTCCAGCGC
5051 ACAGTTAAAT ATGGGGGACG CCAGCAGCTG CCGTTACCTG GTGAAATGAA
5101 TGCTTTTCTG AAAGGGCAAG CAGTTCGTTT GCTTCTAATT CACCTGCCTG
5151 GGGGTGTGGA CTACAGGACG AATTCACAGA CATTACAGT GGCAGGGGAA
5201 GTGCTAGAGG AGCTGTGTGG ACAGATGGGC ATCACAGACT TGAAGAAGT
5251 GCAGGAATTT GCCCTCTTTC TCATCAAAGG AGAAGGTGAG CTGGTTCGGC
5301 CGCTGTCACC CCATGAGTAC ATCAACAATG TGGTGACGGA CCAGGACATG
5351 AGCCTTCACA GCCGACGGCT TGGTTGGGAG ACTCCACTGC ATTTTGATCA
5401 CTCCACCTAC ACGGAAACCC ACTATGGCCA GGTGCTTCGG GACTACCTGC
5451 AAGGGAAGCT GATAGTCAGC ACCCAGGCAG AGGCTCTACT TGCCAGCTT
5501 GCTGCCTTCC AACACTTCGA CAAAACCGGA ACTTCTAGTC CTCCATCAGA
5551 GCAAGAGCTG CTGTCTTATA TTCCCAAGCC ACTGCAATGG CAGGTGAACA
5601 CAGCCAACAT AAAGAGCTTG GTGACCCAGG AGCTGAGGCA GATGCAAGGG
5651 TACAGCAAGC AGAGAGCACA GATTGGCTTT ATAGAGAGCA CAGCGCAGCT
5701 GCCCTCTTTT GGCTACACTG TGTACGTAGT GCTGAGAGTG AGTAAGCTGG
5751 CCCTCCCTGG ACCAGGCCTC CTGGGGCTGA ACCGTCAGCA CCTGGTCCTC

FIG. 2E.

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5801 ATGGACCCCA GCTCTCAGGA ACTCTGCTGC TCTGTCATGC TAAAAGACCT
5851 GAAGCAGTTC CACCTGCTGA GCCCACTGCA GGAGGACGGG CCCCTTGGCC
5901 TAGAACTCAA CTATGGCTCT GTTGACAACC CCCAGACCAT CTGGTTGGAG
5951 TTGCCACAGG CCCAGGAGCT GCAGCACACC ATCATCTTCC TGCTGGGCAG
6001 CATGTCCACT CAGTGGCCAG GTCTCCTCTG AGGAGTGGAG ATAAGGCAGC
6051 GGTCTCTCAC TGGGCAGTCT GCCTTAGTCC TGCTCTGAAT CCGCTGCACA
6101 ACCCCCCACC CCACGTGGAG GCCAAAAGGC AAAGTTGTGT CACCTGGGAG
6151 AATAGGCAGA CACATCCCCT CTGGGGTGGG CTGCAACAGG AGTTGGGGCA
6201 TTTGCTGGCT AGCCCCAGGG AAAATGCCCA CCCAGCTCGA AAGCGGCACA
6251 AGTAAACAC CCAAGGAAAA AAAAAAAAAA AAAAAAAAAA AAA

FIG. 2F.

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1 CGCTGGGACT GTCACCTACC AGGTGCACAA GTTCATAAAC AGAAACAGGG
51 GCCACCTGGA CCCCGCTGTG CTGGAGATGC TCAGGCAGAG CCAGCTGCAG
101 GTGACCTAGC CTTCTTTCA GTCATGGGC AGCCTGTTCC AAGAAGCAGA
151 GCCCCAGGCT GGGACTGAGC AAAACAAACC CACATTGGCC TCTCGATTCC
201 AGCAGACCCT GGGTGACTTG CTAGCTCGGC TAGGCAGCAG GGGCCATGTC
251 TACGTCATCC ACTGTCTCAA TCCCACCCCT GGAAAGATCC CAGGCCTCTT
301 GGACGTGGGG CATGTGGCAG AGCAGCTGCG TCAGGCTGGC ATCCTGGAGA
351 TCATAGGCAC CCGGAGTACC CACTTCCCCG TGCAGTGTG CTTCCAAGTC
401 TTTCTGGCAA GGTTCATGC CCTGGGGTCA GGGAGACAGA AAGCTGCCTC
451 TGACCAGGAG AGGTGTGGTG CCATCCTCAG TGAAGTGCTG GGGGCAGAGT
501 CACCGCTGTA TCATCTTGA GTCACCCAGG TCCTGCTGCA GGAACAGGGC
551 TGGCAGCAGC TAGAACAGCT GTGGGCTCAG CGGCGCTCAC AGGCCCTGCT
601 CACTCTGCAC CGTGGCCTCC GAGCCTGTAT CACCCGGCAG CGCCTCCGTC
651 TCCTGCCCCG GATGCAGGCT CGTGTGCGTG GGCTCCAGGC CAGGAAGCGA
701 TATCTCCAGC GGAGGTCAGC TCTGGGACAG CTGAACACCA TTCTCTAGT
751 GGCCCGGCC CTGCTCCGGA GACGACAGAA GCTACGGTGT GCCCCTGGCC
801 CGCACAGCGG GGAGCCCTGG GGGAAAGTGT CAAATATGGA CCTGGGTGCG
851 TTAGAGATCC CCGCCAGCT GGCTACTCTG CTGGAGAGGG CGGAAGGCCA
901 CCAGGCCTTG CTGACGGGGA GCATCACAGA GTCCCTGCCA CCTGAGGTCC
951 CCGCCCGGCC CAGCCTGACT CTCCTCCAG ACATTGACCA GTTCCCTTC
1001 TCCAGTTTGT TATCCACCAG CTTTCAGAAG CCATTCTGC CTCGACCAGG
1051 GCAGCCACTG GACGAGCCCC TGACGCGGTT AGATGGCGAG AACCCCTCAGC

FIG. 3A.

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1101 AGGCTCTGGA GATCAACAGG GTGATGCTGC GGCTCCTGGG GGAAGGATCT
1151 CTGCAGTCCCT GGCAAGAGCA GACCATGGGC ACGTTCCTCG TGCAGCAGGC
1201 CCAGCGACGG CCGGGACTCC GAGATGAGCT CTTCAGCCAG CTGGTGGCCC
1251 AGCTGTGGCG CAACCCAGAT GAGCAACAGA ATCAGCGTGG CTGGGCCCTA
1301 ATGGTGATCC TGCTCAGCTC CTTTGCTCCC ACACCTGCCC TGGAGAAGCC
1351 ACTGCTCAA TTTGTATCTG ACCAGGCTCC CAGTGGCATG GCAGCCCTGT
1401 GCCAGCACAA GCTGTTAGGT GCCCTGGAGC AGACACCGCT GGCTCCCATG
1451 GCTTCGAGGT CCCACCCACC CACACAACCT GAGTGAAGG CTGGTTTACG
1501 TCGGGGCCGC ATGGCGCTGG ATGTGTTTAC ATTCAACGAG GAAAGCTACT
1551 CCGCGGAAGT GGAATCCTGG ACCACGGGAG AGCAGTTTGC AGGGTGGATC
1601 CTACAGAGCA GAGGCCTGGA GCGCCCCCT CGTGGCTGGT CTGTGCTACT
1651 GCATCTCTGGG GATGCTTGGC GTGACTTGCC TGGCTGTGAC TTTGTGTTGG
1701 ACCTAATAGG CCAGACTGAG GACTTGGGAG ACCCAGCTGG TCCCCACAAC
1751 TACCCCATCA CTCCTCTTGG TTTAGCTGAG AGCATCCCTC CAGCCCCTGG
1801 TGTCCAGGCT CCTTCCCTGC CCCCAGGACT CCCTCCAGGT CCAGCCCCAA
1851 TACTGGCCAG CAGCCGCCCT CCGGGCGAGG CCAGTAAGCC TGAGAACCTG
1901 GATGGTTTCG TGGACCACCT CTTTGAACCA GCGCTCGCTC CGGGTTTCAG
1951 TGATCTGGAA CAAGGCTGGG CCCTGAGCAG ACGCATGAAG GGAGGGGGCT
2001 CTGTTGGGCC CACCCAGCAG GGCTACCCCA TGGTGTACCC AGGTATGGTG
2051 CAGGCACCTA GCTACCAGCC AGCTATGATA CCCGCACCGA TGCCCCGTCAT
2101 GCCAGCCATG GCGCAGTCC CAACCATGCC AGCCATGATG GTGCCACCCC
2151 AGCCACAGCC TCTGGTGCCC AGTTTGGACT CAAGGCAGCT GGCACCTACG
2201 CAGCAAACT TCATCAACCA GCAGGCGATG ATTCTGGCGC AGCAGATGAC
2251 CACCCAGGCC ATGAGCCTGT CCCTGGAGCA GCAGAATCAG AGACACCGAC

FIG. 3B.

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2301 ACCAAGCTCA GACCTCTGGG GCCACCTCCC AGCCTCCACC CTCAACCACT
2351 GCTCCCAAGG CCAAGAAGCC TCCTGCCCCC CAAGAGAAGC CAGAGAGTAA
2401 CCTAGAGCCT TCGGGTGTG GCTTGAGAGA GGACACCCCA GAGGAAGCTG
2451 AAAGCAAGCC TCAGCGCCCC AAGAGCTTCC AACAGAAACG GGACTATTTT
2501 CAGAAGATGG GGCAAGATCC GATCAGAGTG AAGACGGTGA AACCTCCAGC
2551 CAAGGTTTAC ATCCCCAAG AGGAGATGGA GGAGACGGAG GAGGAGGAGG
2601 ATGAGACCGC CGAGTTGTCC CCTCCTCTC CCCCTCCCC GGTGTGAAG
2651 AAGCCGCTGA AGGCAAGCAG GCCCAAAGCC GTAAAGGAAG ATGAGGCAGA
2701 GCCCCCCCAG GAGGAAGTAC CGACCCAGGG CGAGGATCCC CCGGTGCACA
2751 GCTCCAATC CGCACCTCAG CACCCCAAAC CCAGCAGGGT ACCCCAGTG
2801 CAGAGCTCCA ACTCCGCACC TCCACGCCCG CAACCCAGCA GGGAAATCCG
2851 AAACATCATC CGAATGTACC AGAGCCGTCC AGGGCCTGTG GCTGTGCCCC
2901 TACAACCCAC CAGGCCCATC AAAACTTTTC AGAAGAAAAA TGACCCTAAG
2951 GATGAGGCTT TGGCTAAGTT AGGGATAAAT GGCCTCCACT TGCCCTATC
3001 GACATCGCCT AACCAAGGGA AGAGCTCTCC ACCGGCTGTA GTTCTCGAC
3051 CTAAGGCTCG ACCTCGTCTT GAGCCTTCCC TATCCATCCA GGAAAAGCAG
3101 GGACCCTTTC GGGACTTGTT TGGCCCATGT AGTCCAAACC CACCTACAGC
3151 TCCAGCACCC CCGCCTCCAC CAGCACTCCC ACCGCCTCTG TCTGGGGAGC
3201 CCAAGACCCC TTCAGTGGAG TCTCATGCCT TGACAGAGCC CATGGAGGAC
3251 AAGAACATCT CCACAAAGCT CCTTGTGCCC TCTGGAAGTG TGTGCTTCTC
3301 CTATGCCAAT GCACCCTGGA AGTTGTTCTT ACGCAAGGAG GTGTCTTACC
3351 CCCGGGAGAA CTTCACTCAT CCATACTGCC TCAGTCTCCT CTGCCAGCAG
3401 ATCCTGCGGG ACACCTTCAC AGAGTCTGC ACCCGGATCT CACAGGATGA

FIG. 3C.

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3451 GCGGCACAAA ATGAAAGGCC TTCTGGGAGA CTTGGAGGTG AGTCTGGAGA
3501 CCCTTGACAT TGTTGAAGAC AGCATCAAAA AACGCATCGT GGTGCGTGCT
3551 CGGGACAAC TGGCCAATTA CTTCTCCCGC ATCTTCCAG TCTCGGGTGA
3601 GAGTGGCAGC GATGTACAGC TGCTGGGTGT GTCTACCGG GGAAGTGGGC
3651 TGCTGAAGGT GACCCAAAGC CCGAGCTTCC ACCTGGACCA GCTGAAGACA
3701 CTCTGTTTCT ACAGCTATGC TGAAGTCCTG ACCGTGCAGT GCAGGGGACG
3751 ATCCACCCTG GAGCTGTCCT TGAAGAATGA GCAGCTGATA CTGCACACAG
3801 CCTGGGCGAG GGCCATCAAG GCCATGGTGG ATCTATTCTT GAGTGAACCT
3851 AGGAAGGACT CCGGCTATGT CATCGCCCTG CGCAGCTACA TCACCGATGA
3901 CAATAGCCTC CTCAGTTTCC ACCGTGGGGA CCTCATTAGG TTAAGTCCAG
3951 TGACCGCTCT GGAACCAGGC TGGCAGTTCG GTTCTGCCGG GGGCCGCTCC
4001 GGACTCTTTC CCGATGACGT GGTGCAGCCA GCTGCTGCCC CCGACCTCTC
4051 CTTTTCCCTG GGAAGAGAGAA ACAGCTGGCA ACGCAAGAGT AAGCTGGGGC
4101 CAGCTCAGGA GGTGAGGAAG ACAGAAGAGG TGAAGTATA CAGGCCTAAC
4151 TTGGAGACTG AGAAGGAAAG AGCAGGGTTG CTTCCGGGTG TGTCCACTTC
4201 CTGTCCTGGT GGCCAGGGCT CAATGTGTTC CTGTCCTTTA CCATCTCCTG
4251 ACTTTTTGCC ATTTGTGAGA CTGTAAGTCA CACCCTCTAA CTCTGGTACT
4301 TAGTTCAGTG TCTCCATAGA GGATGCTTAA TAAATAACCT TGGTTTTCCT
4351 GGAAAAAAAA AAAAAAAAAA AAAAA

FIG. 3D.

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MYQSRPGVPVPVQPSRPPKAFLRKIDPKDEALAKLGINGAHSPMLSPSGKGPFPVAVRPKA
PLQLGPSSTIKEKQGPLLDLFGQKLPIAHTPPPPAPPPLPEDEPGTISAERRCLTPVEDQGVST
QLLAPSGSVCSYTGTPWKLFTRKEVEYPRENFSPYLRLLCEQILRDTFESCIRISQNERRKM
KDLLGGLEVDLSLTTEDSVKKRIVVAARDNANYFSRFFVSGESGSDVQLLAVSHRGLRLKV
TQGFGLRPDQKILCSYFAEVLGVECRGGSTLELSKSEQVLHTARAEALVELFILNELKKD
SGYVIALRSYITDNCSSLSSFHRGDLIKLLPVATLEPGWQFGSAGRSGLFPADIVQPAAPDFSFS
KEQRSGWHKGQLSNGEPGLARWDRASEVRKMGEGQAEARPA

FIG. 4.

FIG. 5A.

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TCCCACGTGGTACTTAGTTCAAGGCTGCCCCAGCAGATGCTTAATAAACAGCTCTTCACTTTCTCTG
GCTTCTGGTCTTGCTCCTTTGGTGTCTGGCTGGGGAGGGATGGGGCTGGGGCAGGACCCCTGGGAC
AGGGCACTGGACACTCAGGTGGCACCAGGTTTCTTGATCCAGCGCCCTGCCACCCCTGGAGC
CAGGCACACAGTGACGACTCGGAGGCCACCAGCCTGTCTCTGTGGCCTATGCCTTTCTGCCCGAC
TCCCACAGTACACCATGCAGGAATTGCCCCGGCGTTACTTCCGGAGGTCCCAGGCCTTGCTGGGC
CAGACTGATGGAGGTGCCGAGGAAGGACACGGACAGCCTGGTGCAGTACACCAAGGCTCCCATC
CAGGAGTCGCTCCTCAGCCTCAGTGATGATGTGAGCAAGCTGGCTGTAGCCAGCTTCTTGCCCTC
GATGCGGTTTATGGGTGACCAGTCCAAGCCCCGGGCAAGGATGAGATGGATCTGCTCTATGAACT
GCTGAAGCTGTGCCAGCAGGAGAAGCTGAGGGATGAGATTACTGCCAGGTTATCAAGCAGGTCAC
AGGACACCCCCGGCCGGAACACTGCACTCGAGGCTGGAGCTTCTCTCAGCCTTCTCACAGGCTTCTT
CCCCCGCTCGACACAGGCTGATGCCCTACCTGACCAAGTTTCTGCGAGGATTCAGGCCCCAGCCAAGA
GCTGGCCCCGGAGCAGCCAGGAGCACCTCCAGCGCACAGTCAAATATGGGGGGCGCCGGCGGATGCC
CCCACCGGGTGAAATGAAGCTTTCTTGAAAGGACAAGCGATTTCGCCTGCTTCTTATCACCTGCC
GGGGGGTGTGGATTATAGGACGAATATCCAGACTTTACAGTAGCAGAGTGCAGGAGGAGCT
GTGCCGCGCAAATGGGTATCACGGAGCCTCAGGAAGTGCAGGAATTCGCCCTCTTCCTCATCAAAGA
GAAGAGCCAGCTGGTGCGGCCCCTGACGCCCGCCGAATACCTCAACAGCGTGGTAGTGACACAGGA
CGTGAGCCTGCACAGCCGGCGGCTCCACTGGGAGACCCACTGCACTTCGATAACTCCACCTACAT
CAGCACCCACTACAGCCAGGTGCTGTGGGACTACCTTCAGGGGAAGCTGCCAGTCAGCGCCAAGGC
AGACGCGCAGCTCGCCAGGCTGGCCGCCCTGCAGCACCTCAGCAAGGCCAACAGGAATACCCCTC
AGGGCAGGACCTGTAGCTTACGTGCCAAAGCAGCTGCAACGGCAGGTGAACACGGCCTCCATCAA
GAACCTGATGGGTGAGGAGCTGAGACGGCTGGAAGGACACAGCCCCAGGAAGCACAGATCAGCTT
CATTGAGGCCATGAGCCAGCTGCCCTCTTCGGCTACACCGTCTATGGGGTGTGCGAGTGAGCAT
GCAGGCCCTGTCCGGACCCACTCTCCTGGGGCTCAACCGCCAGCATCTCATCCTCATGGACCCAG
CTCCCAGAGCCTGTACTGCCGATTGCCCTGAAGAGCCTGCAGCGGCTCCACCTGCTAAGCCCTCT
GGAGGAGAAGGGGGCCCCCTGGCCTGGAAGTCAACTATGGCTCAGCTGACAACCCCCAGACCATCTG
GTTTGAGCTGCCACAGGCCAGGAGCTGCTATACACCAGCTGTCTTCCTGATAGACAGCAGTGCCCTC
TTGCACTGAGTGGGCCAGCATCAACTGAGAGGAGTGACGGCCGGGAGAGAAGAGGATGAGGCCCTC
CCCCGGCCCAAGTCTCACCCACATGGTCTGCCTTGGATGCTATCAGATCACTGTCTTAGAACCTGC
CTCAGCACAGCCCAGCGGCCACATGCAGGCCATGAGGCAGGGGCTGCTATCAGTCAACAGCAG
GCAAAGAAAACAGCCAGACCCCTCTCCAGGACGGCTGGGGCCAAAGCGGGCTGCAGGAACCTCGCT
GGGGCACCTGAGGTGCCAGTCTGAGGAGATGCCACCCGACCCAGGCTCCGCCAGGCCCCA

FIG. 5B.

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CATTAGCACAAAGCCAGGCATGGGAGAAACAGCTGCTGAGGAAATAAACTCCCTAAAAAAAAAAAA
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FIG. 5C.

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MYQSRPGVPVPVQPSRPPKAFLRKIDPKDEALAKLINGAHSSPMLSPSPGKGPPPAVAPRPKA
PLQLGPSSSIKEKQGPLLDLFGQKLPIAHTPPPPAPPLPLPEDPGTLSAERRCLTQVEDQGVST
QLLAPSGSVCFSYTGTPWKLFRLKEVFYPRENFHSHYYLRLLCEQILRDTFSESCIRISQNERRKM
KDLLGGLEVLDLSLTTTEDSVKKRIVVAARDNWANYFSRFFPVSGESGSDVQLLAVSHRGLRLLKV
TQGFGLRPDQLKILCSYSFAEVLGVECRGGSTLELSLKSEQLVLHTARARAIEALVELFLNELKKD
SGYVIALRSYITDNCSLLSFHRGDLIKLLPVATLEPGWQFGSAGGRSGLFPADIVQAAAPDFSFS
KEQRSGWHKQQLSNGEPGLARWDRASERPAHPWSQAHSDDEATSLSSVAYAFLPDSHSYTMQEF
RRYFRRSQALLGQTDGGAAGKDTDSLVQYTKAPIQESLLSLSDDVSKLAVASFLALMRFMGDQSKP
RGKDEMDLLYELLKLCQKEKLDEIYCQVIKQVTGHPPEHCTRGSFSLTGTGFFPPSTRLMPYL
TKFLQDSGPSQELARSSQEHLQRTVKYGGRRRMPPPGEMKAFLKGQAIRLLLIHLPGGVDYRTNIQ
TFTVAEVQEELCRQMGITEPQEVQEFALFLIKEKSQVLVRPLQPAEYLNVSVVDDQDVSLSHGGSTG
RPHCTSIPTPTAPTARCCGTTFRGSCQSAPRQTRSSPGWPPCSTTSARPTGIPPGQRTG

FIG. 6.

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FIG. 7A.

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TCCAGGAGTCGCTCCTCAGCCTCAGTGATGATGTGAGCAAGCTGGCTGTAGCCAGCTTCTGGCCC
TGATGCGGTTTATGGGTGACCAGTCCAAGCCCCGGGGCAAGGATGAGATGGATCTGCTCTATGAAC
TGCTGAAGCTGTGCCAGCAGGAGAAGCTGAGGGATGAGATTTACTGCCAGGTTATCAAGCAGGTCA
CAGGACACCCCCGGCCGGAACACTGCACTCGAGGCTGGAGCTTCTCAGCCTTCTCACAGGCTTCT
TCCCCCGTCGACCAGGCTGATGCCCTACCTGACCAAGTTTCTGCAGGATTCAGGCCCCAGCCAAG
AGCTGGCCCCGAGCAGCCAGGAGCACCTCCAGCGCACAGTCAAATATGGGGGGCGCCGGCGGATGC
CCCCACGGGTGAAATGAAGGCTTTCTGAAAGGACAAGCGATTTCGCCTGCTTCTTATTACCTGTC
CGGGGGGTGTGGATTATAGGACGAATATCCAGACTTTCACAGTAGCAGCAGAAGTGCAGGAGGAGC
TGTGCCGGCAAATGGGTATCACGGAGCCTCAGGAAGTGCAGGAATTTCGCCCTCTTCTCATCAAAG
AGAAGAGCCAGCTGGTGGCGGCCCTGCAGCCCGCCGAATACCTCAACAGCGTGGTAGTGGACCAGG
ACGTGAGCCTGCACAGCGGGCGGCTCCACTGGGAGACCCCACTGCACCTCGATAACTCCACCTACAT
CAGCACCCACTACAGCCAGGTGCTGTGGGACTACCTTCAGGGGAAGCTGCCAGTCAGCGCCAAGGC
AGACGCGCAGCTCGCCAGGCTGGCCGCCCTGCAGCACCTCAGCAAGGCCAACAGGAATACCCCTC
AGGGCAGGACCTGCTAGCTTACGTGCCAAAGCAGCTGCAACGGCAGGTGAACACGGCTCCATCAA
GAACCTGATGGGTGAGGAGCTGAGACGGCTGGAAGGACACAGCCCCAGGAAGCACAGATCAGCTT
CATTTAGGCCATGAGCCAGCTGCCCCCTCTTCGGCTACACCGTCTATGGGGTGCTGCGAGTGAGCAT
GCAGGCCCTGTCCGAGCCCACTCTCCTGGGGCTCAACCGCCAGCATCTCATCTCATGGACCCAG
CTCCAGAGCCTGTACTGCCGATTTGCCCTGAAGAGCCTGCAGCGGCTCCACCTGCTAAGCCCTCT
GGAGGAGAAGGGGGCCCCCTGGCCTGGAAGTCAACTATGGCTCAGCTGACAACCCCCAGACCATCTG
GTTTGAGCTGCCACAGGCCAGGAGCTGCTATACACCACTGTCTTCTGATAGACAGCAGTGCCTC
TTCACCTGAGTGGCCAGCATCAACTGAGAGGAGTGCAGGCCGGGGAGAGAAGAGGATGAGGCTC
CCCCGGCCCCAAGTCTCACCCACATGGTCTGCCTTGGATGCTATCAGATCACTGTTCTAGAACCTGC
CTCAGCACAGCCCAGCGGCCACATGCAGGCCATGAGGCAGGGGCTGCTATCAGCTCACCAGCAG
GCAAGAAAAACAGCCAGACCTCTCCAGGACGGCCTGGGGCCAAGCGGGCTGCAGGAACCTCGGCT
GGGGCACCTGAGGTTGCCAGTCTGAGGGAGATGCCACCCGACCCAGGCTCCGCCAGGCCCCCA
CATTAGCACAGCCCCAGGCATGGGAGAAACAGCTGCTGAGGAAATAAACTCCCTAAAAA
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FIG. 7B.

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mMRP: 914 MYQSRGPGVAVPVQTRPIKTFQKNDRPKDEALAKINGVHL-PLSTSPNOGKSSPPAV 972
MYQRGPGV PVQGRP K +K DKPKDEALAKING H P SP+ GK PPVAV
hmRP: 1 MYQSRGPGVAVPVQSRPPKATLKIDPKDEALAKINGAHSPMLSPSEGGKPPAV 60

mMRP: 973 VPRKAPRLSESLSTQEKQGLRDLEGPCSNPTAPAPPPPPALPPLSGEPKTSVE 1032
PRPKA +L PS SI+EQGEL DLEFG P A PPPPA P PL +P T S E
hmRP: 61 APRKAPLQLGSSSIKENQGLDLFGQ---KLEIAHTPPPPAPPPELPEDEPGTISAE 117

mMRP: 1033 SHAUTERMEDKNISTKLLVPSGVCFSYANAPWKFLRKEVEYPRENFSPYCLSLICQ 1092
IT+P+ED+ +ST+LL PGSVCFYSY PWKFLRKEVEYPRENFSPY L LIC+Q
hmRP: 118 RRCLTQVEDQGVSTQLLAPSGVCFSTGTGTPWKFLRKEVEYPRENFSPYLLICEQ 177

mMRP: 1093 ILRDTFTESCIRISODERHKMGLLGLEVSLFTLIDIVEDSIRKRIIVAAARONWANVESR 1152
ILRDTF+ESC RISQ+ER KMK LLG LEV L++L EDS+KKRIIVAAARONWANVESR
hmRP: 178 ILRDTFESCIRISQNERAKMDLLGLEVDLSITTTEDSVYKRIIVAAARONWANVESR 237

mMRP: 1153 IFPVSGESGDVQLLGVSHRGLRLKVTQSPSEHLDQLKILCSYSAEVLTVQCRGSTL 1212
FPVSGESGDVQLL VSHRGLRLKVTQ P DQLK LCYS+AEVL V+CRG STL
hmRP: 238 IFPVSGESGDVQLLAVSHRGLRLKVTQGPGLREDPQLKILCSYSAEVLGVCEGSGSTL 297

mMRP: 1213 ELSLKNQLLHTAWARAIAKMDVLFSELKDSGYIALRSYITDONSLLSEHFGDLIR 1272
ELSLK+QOL-LHTA ARAI+A+V+LFL+EL+KDSGYIALRSYITD+ SLLSEHFGDLI+
hmRP: 298 ELSLKSQVLHTARARATEALVELFTNELKDSGYIALRSYITDNGSLLSEHFGDLIK 357

mMRP: 1273 LLPVTALEPGWFGSAGRSGLFPDDVYVQPARAPDLSESLGKNSMR 1320
LLPV LEPGWFGSAGRSGLFP D+VQPARAPD SFS +R+ W +
hmRP: 358 LLPVATLEPGWFGSAGRSGLFPADIVQPARAPDSEFSKEQSGMWHK 405

Identities = 302/408 (74%), Positives = 334/408 (81%), Gaps = 4/408 (0%)

FIG. 8.

132709 03710049

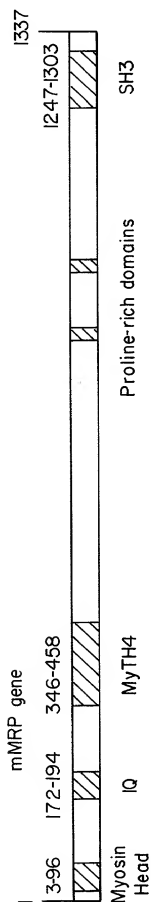


FIG. 9.

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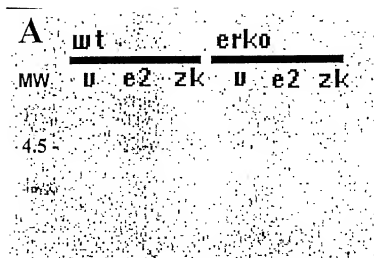


FIG. 10.

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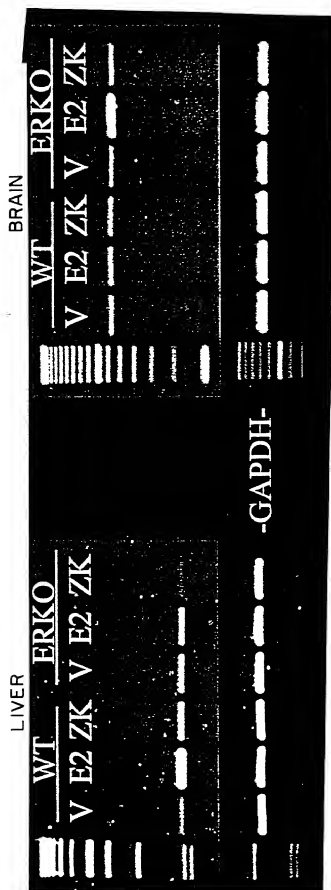


FIG. 11.

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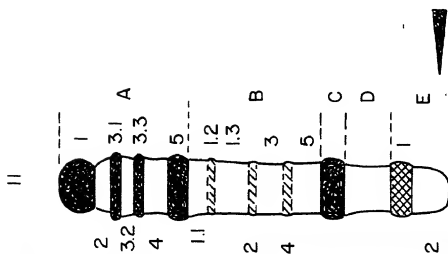


FIG. 12.

